

10 30 50
 TCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTGTCAGTGTG
 M R L S V C
 70 90 110
 CTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGCCAGCT
 L L M V S L A L C C Y Q A H A L V C P A
 130 150 170
 GTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAAGTT
 V A S E I T V F L F L S D A A V N L Q V
 190 210 230
 GCCAACTTAATCCACCTCCAGAAGCTCTTGAGCCAAGTTGGAAGTGAAGCACTGCACC
 A K L N P P P E A L A A K L E V K H C T
 250 270 290
 GATCAGATATCTTTAAGAAACGACTCTCATTGGAAAAAGTCCTGCGTGAATAAGTGA
 D Q I S F K K R L S L E K V L V E I V K
 310 330 350
 AAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCAAAGTCTTTCAACGACAC
 K C G V
 370 390 410
 CCTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCC
 430
 TGCACATCAAAAA

FIG.1

10 30 50
 TTGTTTGTGAAAGCTGAGCTCACAGCAAAACAAGCCACCATGAAGCTGTGCGTGTGTCTC
 M K L S V C L
 70 90 110
 CTGCTGGTCACGCTGGCCCTCTGCTGCTACCAGGCCAATGCCGAGTTCTGCCAGCTCTT
 L L V T L A L C C Y Q A N A E F C P A L
 130 150 170
 GTTTCTGAGCTGTTAGACTTCTTCTTATTAGTGAACCTCTGTTCAAGTTAAGTCTTGCC
 V S E L L D F F F I S E P L F K L S L A
 190 210 230
 AAATTTGATGCCCCTCCGGAAGCTGTTGCAGCCAAGTTAGGAGTGAAGAGATGCACGGAT
 K F D A P P E A V A A K L G V K R C T D
 250 270 290
 CAGATGTCCCTTCAGAAACGAAGCCTCATTGCGGAAGTCCTGTTGAAAATATTGAAGAAA
 Q M S L Q K R S L I A E V L V K I L K K
 310 330 350
 TGTAGTGTGTGACATGTAAAACTTTCATCCTGGTTTCCACTGTCTTTCAATGACACCCCT
 C S V
 370 390 410
 GATCTTCACTGCAGAATGTAAAGGTTTCAACGTTGCTTTAATAAATCACTTGCTCTCC
 430
 AAAAAAAAAAAAAA

FIG.2

10 30 50
 ACGAGCTGCCACGCACGACTGAACACAGACAGCAGCCGCTCGCCATGAAGCTGCTGATG
 M K L L M
 70 90 110
 GTCCTCATGCTGGCGGCCCTCCTCCTGCACTGCTATGCAGATTCTGGCTGCAAACCTCTG
 V L M L A A L L L H C Y A D S G C K L L
 130 150 170
 GAGGACATGGTTGAAAAGACCATCAATTCCGACATATCTATACCTGAATACAAAGAGCTT
 E D M V E K T I N S D I S I P E Y K E L
 190 210 230
 CTTCAAGAGTTCATAGACAGTGATGCCGCTGCAGAGGCTATGGGAAATTCAAGCAGTGT
 L Q E F I D S D A A A E A M G K F K Q C
 250 270 290
 TTCCTCAACCAGTCACATAGAACTCTGAAAACTTTGGACTGATGATGCATACAGTGTAC
 F L N Q S H R T L K N F G L M M H T V Y
 310 330 350
 GACAGCATTGGTGTAATATGAAGAGTAATTAACCTTTACCCAAGGCGTTTGGCTCAGAGG
 D S I W C N M K S N *
 370 390 410
 GCTACAGACTATGGCCAGAACTCATCTGTTGATTGCTAGAAACCACTTTCTTCTTGTT
 430 450 470
 GCTTTTATGTGGGAACTGCTAGACAACCTGTTGAAACCTCAATTCATTCCATTCA

FIG.3

1 MRLSVCLLMVSLALCCYQAHA.LVCPAVASEITVFLFLSDAAVNQLQAKL 49
 : ||:||||:: ||:||||:|:| :|. || |.. ||: |:.... :....
 4 ielslcllim.lavccyeanosqicelvohetisflmkseeelkkelemy 52
 50 NPPPEALAAKLEVKHCTDQISFKRLSLEKVLVEIVKKCGV 90
 |:|:|.|||:|:|.||:| .|| :...|| |. .|||
 53 nappaaveaklevkrctvdqmsngdr lvvaetlvvifilecgv 93

FIG.4

1 MKLSVCLLLVTLALCCYQANA.EFCPALVSELLDFFFISEPLFKLSLAKF 49
 :.||:||||:: ||:||||:|||| ::|. :. | :. |: ||. :| .|.:
 4 ielslc||im.lavccyeanasqicelvahtisflmkseeelkkelemy 52

50 DAPPEAVAAKLGVKRCTDQMSLQKRSLIAEVLVKILKKCSV 90
 :||||.||.||||:||||.|||| ..| ::||.|| | : .|:|
 53 nappaaveaklevkr cvdqmsngdr lvvaetlv yif leagv 93

FIG.5

1 MKLLMVLMLAALLLHCYA.DSGCKLLEDMEKTINSDISIPEYKELLQEF 49
 |||:|:::|... : ||| :|||.:|::: |||:|:::|...|...:
 1 mklvf|||lvtipiccyasgsgsildevirgtinstvtlhdymklvkpy 50

50 IDSDAAAEAMGKFQKCFLNQSHRTLKNFGLMMHTVYDSIWCNMKSN 95
 :... ..|: .|||||:|...||.|. |:|...:| .|. .|
 51 vgahftekavkqfkqcfldqtdktl envgvmmeaifnse scqpps. 95

FIG.6

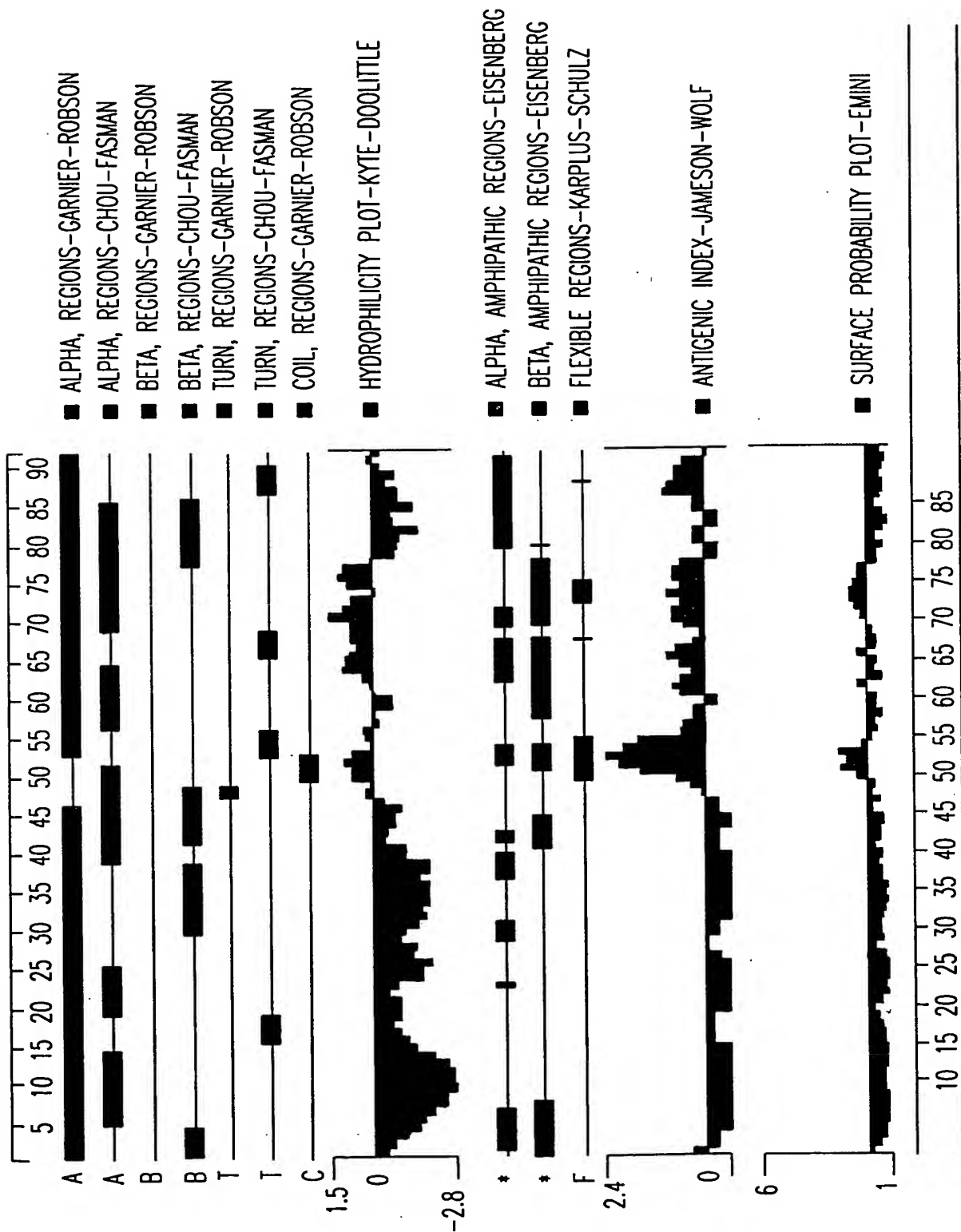


FIG.7

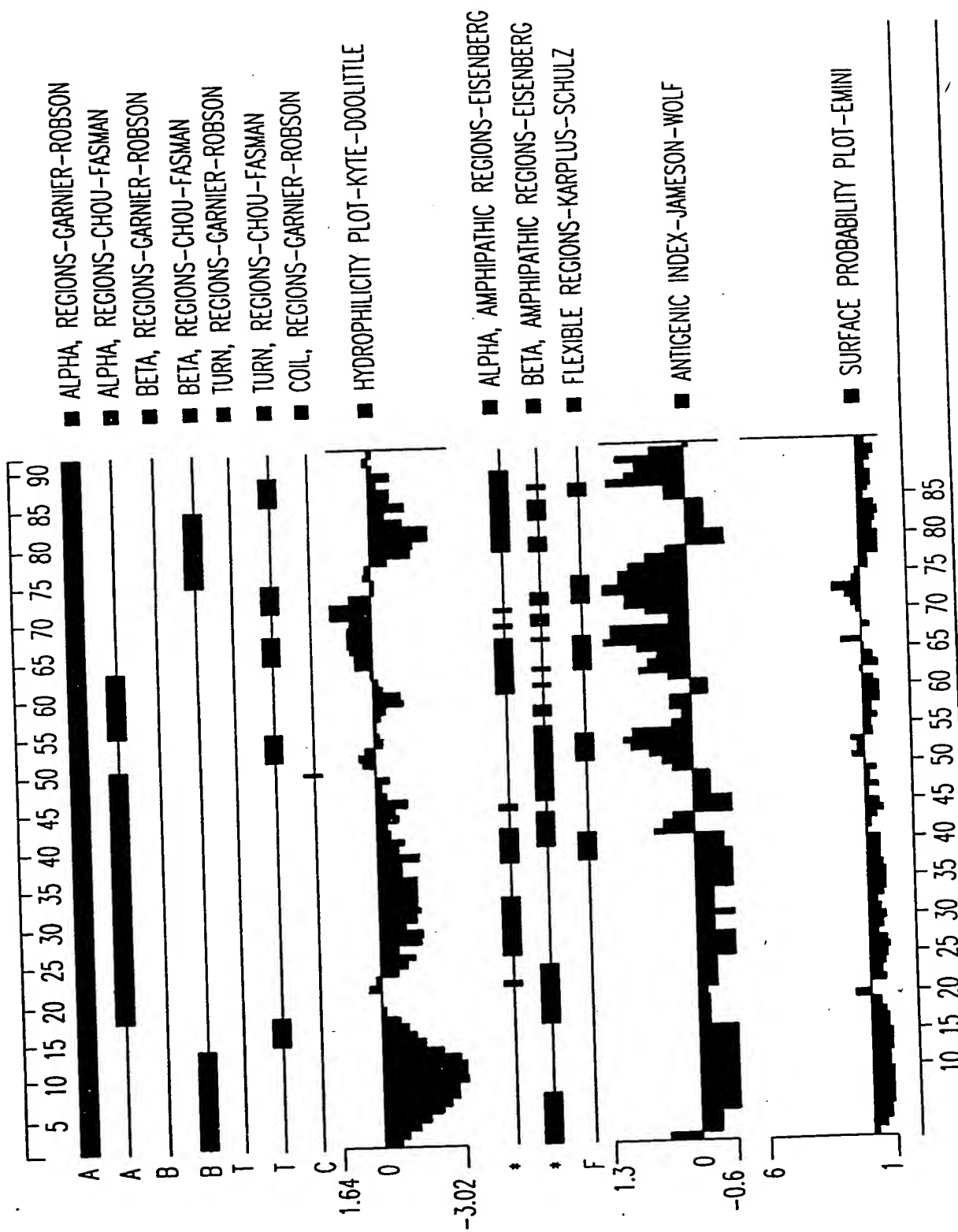


FIG. 8

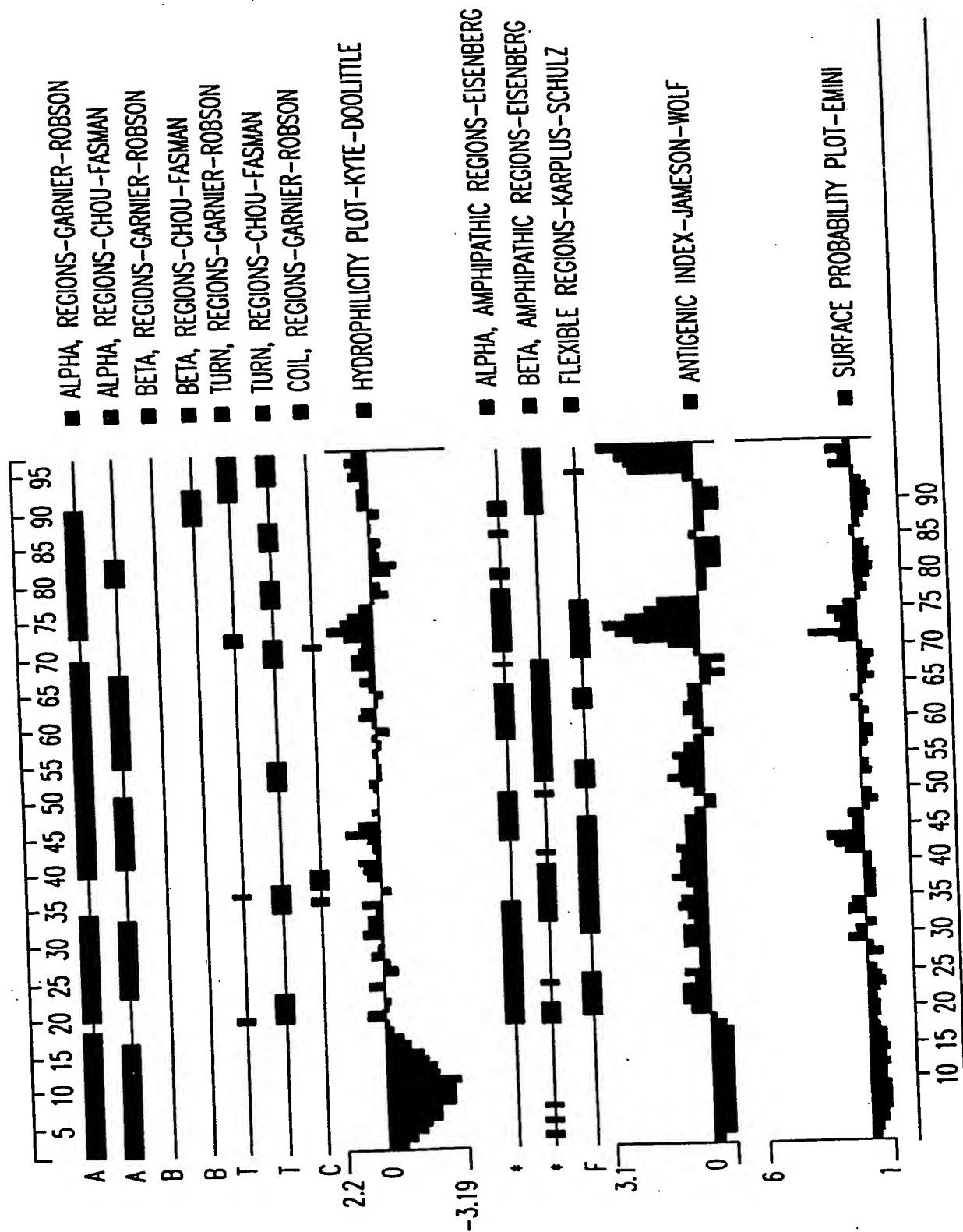


FIG.9